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## RAW SEQUENCE LISTING

DATE: 03/01/2002

PATENT APPLICATION: US/10/072,436

TIME: 11:01:01

Input Set : A:\1803.txt

Output Set: N:\CRF3\03012002\J072436.raw

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5 <110> APPLICANT: MARKAU, URSULA
7     EBENBICHLER, CHRISTINE
9     ACHHAMMER, GUNTAR
11    ANKENBAUER, WALTRAUD
15 <120> TITLE OF INVENTION: MODIFIED DNA-POLYMERASE FROM CARBOXYDOTHENUS
HYDROGENOFORMANS AND
16    ITS USE FOR COUPLED REVERSE TRANSCRIPTION AND POLYMERASE CHAIN REACTION
20 <130> FILE REFERENCE: 1803-332-999
C--> 23 <140> CURRENT APPLICATION NUMBER: US/10/072,436
C--> 23 <141> CURRENT FILING DATE: 2002-02-05
23 <150> PRIOR APPLICATION NUMBER: 09/204,208
25 <151> PRIOR FILING DATE: 1998-12-01
29 <150> PRIOR APPLICATION NUMBER: EP 97121151.1
31 <151> PRIOR FILING DATE: 1997-12-02
35 <160> NUMBER OF SEQ ID NOS: 12
39 <170> SOFTWARE: PatentIn version 3.0
43 <210> SEQ ID NO: 1
45 <211> LENGTH: 18
47 <212> TYPE: DNA
C--> 49 <213> ORGANISM: Artificial
51 <220> FEATURE:
53 <223> OTHER INFORMATION: Description of artificial sequence: amplification primer
57 <220> FEATURE:
59 <221> NAME/KEY: misc_feature
61 <222> LOCATION: (3)..(3)
63 <223> OTHER INFORMATION: any nucleotide
67 <220> FEATURE:
69 <221> NAME/KEY: misc_feature
71 <222> LOCATION: (9)..(9)
73 <223> OTHER INFORMATION: any nucleotide
77 <400> SEQUENCE: 1
W--> 78 ccnaaytnc araayath 18
81 <210> SEQ ID NO: 2
83 <211> LENGTH: 15
85 <212> TYPE: DNA
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89 <220> FEATURE:
91 <223> OTHER INFORMATION: Description of artificial sequence: amplification primer
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97 <221> NAME/KEY: misc_feature
99 <222> LOCATION: (10)..(10)
101 <223> OTHER INFORMATION: any nucleotide
105 <400> SEQUENCE: 2
W--> 106 ytcrtcrtgn acytg 15

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109 <210> SEQ ID NO: 3
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117 <220> FEATURE:
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124 gggcgaagac gctatattcc tgagc 25
127 <210> SEQ ID NO: 4
129 <211> LENGTH: 28
131 <212> TYPE: DNA
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135 <220> FEATURE:
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142 gaagccttaa ttcaatctgg gaataatc 28
145 <210> SEQ ID NO: 5
147 <211> LENGTH: 36
149 <212> TYPE: DNA
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155 <223> OTHER INFORMATION: Description of artificial sequence: amplification primer
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178 cgaattcaag gatccttact tcgcttcata ccagtt 36
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185 <212> TYPE: DNA
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189 <220> FEATURE:
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195 <400> SEQUENCE: 7
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201 <211> LENGTH: 39
203 <212> TYPE: DNA
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209 <223> OTHER INFORMATION: Description of artificial sequence: amplification primer
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217 <210> SEQ ID NO: 9

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219 <211> LENGTH: 26
221 <212> TYPE: DNA
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225 <220> FEATURE:
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235 <210> SEQ ID NO: 10
237 <211> LENGTH: 1824
239 <212> TYPE: DNA
241 <213> ORGANISM: Carboxydothermus hydrogenoformans
245 <220> FEATURE:
247 <221> NAME/KEY: CDS
249 <222> LOCATION: (1)..(1824)
253 <400> SEQUENCE: 10
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255 Met Glu Lys Leu Ala Glu His Glu Asn Leu Ala Lys Ile Ser Lys Gln
256 1 5 10 15
258 tta gct aca atc ctg cgg gaa ata ccg tta gaa atc tcc ctg gaa gat 96
259 Leu Ala Thr Ile Leu Arg Glu Ile Pro Leu Glu Ile Ser Leu Glu Asp
260 20 25 30
262 tta aaa gtt aaa gaa cct aat tat gaa gaa gtt gct aaa tta ttt ctt 144
263 Leu Lys Val Lys Glu Pro Asn Tyr Glu Glu Val Ala Lys Leu Phe Leu
264 35 40 45
266 cac ctt gag ttt aaa agc ttt tta aaa gaa ata gaa cca aaa ata aag 192
267 His Leu Glu Phe Lys Ser Phe Leu Lys Glu Ile Glu Pro Lys Ile Lys
268 50 55 60
270 aaa gaa tac cag gaa ggt aaa gat ttg gtg caa gtt gaa act gta gaa 240
271 Lys Glu Tyr Gln Glu Gly Lys Asp Leu Val Gln Val Glu Thr Val Glu
272 65 70 75 80
274 acg gaa gga cag att gca gta gtt ttt agt gat gga ttt tat gtt gat 288
275 Thr Glu Gly Gln Ile Ala Val Val Phe Ser Asp Gly Phe Tyr Val Asp
276 85 90 95
278 gac ggg gaa aaa aca aag ttt tac tct tta gac cgg ctg aat gaa ata 336
279 Asp Gly Glu Lys Thr Lys Phe Tyr Ser Leu Asp Arg Leu Asn Glu Ile
280 100 105 110
282 gag gaa ata ttt agg aat aaa aaa att att acc gac gat gcc aaa gga 384
283 Glu Glu Ile Phe Arg Asn Lys Lys Ile Ile Thr Asp Asp Ala Lys Gly
284 115 120 125
286 att tat cat gtc tgt tta gaa aaa ggt ctg act ttt ccc gaa gtt tgt 432
287 Ile Tyr His Val Cys Leu Glu Lys Gly Leu Thr Phe Pro Glu Val Cys
288 130 135 140
290 ttt gat gcg cgg att gca gct tat gtt tta aac ccg gcc gac caa aat 480
291 Phe Asp Ala Arg Ile Ala Ala Tyr Val Leu Asn Pro Ala Asp Gln Asn
292 145 150 155 160
294 ccc ggc ctc aag ggg ctt tat cta aag tat gac tta ccg gtg tat gaa 528
295 Pro Gly Leu Lys Gly Leu Tyr Leu Lys Tyr Asp Leu Pro Val Tyr Glu
296 165 170 175
298 gat gta tct tta aac att aga ggg ttg ttt tat tta aaa aaa gaa atg 576

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| 299 | Asp | Val | Ser | Leu | Asn | Ile | Arg | Gly | Leu | Phe | Tyr | Leu | Lys | Lys | Glu | Met |      |
| 300 |     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |      |
| 302 | atg | aga | aaa | atc | ttt | gag | cag | gag | caa | gaa | agg | tta | ttt | tat | gaa | ata | 624  |
| 303 | Met | Arg | Lys | Ile | Phe | Glu | Gln | Glu | Gln | Glu | Arg | Leu | Phe | Tyr | Glu | Ile |      |
| 304 |     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |      |
| 306 | gaa | ctt | cct | tta | act | cca | gtt | ctt | gct | caa | atg | gag | cat | acc | ggc | att | 672  |
| 307 | Glu | Leu | Pro | Leu | Thr | Pro | Val | Leu | Ala | Gln | Met | Glu | His | Thr | Gly | Ile |      |
| 308 |     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |      |
| 310 | cag | gtt | gac | cgg | gaa | gct | tta | aaa | gag | atg | tcg | tta | gag | ctg | gga | gag | 720  |
| 311 | Gln | Val | Asp | Arg | Glu | Ala | Leu | Lys | Glu | Met | Ser | Leu | Glu | Leu | Gly | Glu |      |
| 312 | 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |      |
| 314 | caa | att | gaa | gag | tta | atc | cgg | gaa | att | tat | gtg | ctg | gcg | ggg | gaa | gag | 768  |
| 315 | Gln | Ile | Glu | Glu | Leu | Ile | Arg | Glu | Ile | Tyr | Val | Leu | Ala | Gly | Glu | Glu |      |
| 316 |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |      |
| 318 | ttt | aac | tta | aac | tcg | ccc | agg | cag | ctg | gga | gtt | att | ctt | ttt | gaa | aaa | 816  |
| 319 | Phe | Asn | Leu | Asn | Ser | Pro | Arg | Gln | Leu | Gly | Val | Ile | Leu | Phe | Glu | Lys |      |
| 320 |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |     |      |
| 322 | ctt | ggg | ctg | ccg | gta | att | aaa | aag | acc | aaa | acg | ggc | tac | tct | acc | gat | 864  |
| 323 | Leu | Gly | Leu | Pro | Val | Ile | Lys | Lys | Thr | Lys | Thr | Gly | Tyr | Ser | Thr | Asp |      |
| 324 |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |     |      |
| 327 | gcg | gag | gtt | ttg | gaa | gag | ctc | ttg | cct | ttc | cac | gaa | att | atc | ggc | aaa | 912  |
| 328 | Ala | Glu | Val | Leu | Glu | Glu | Leu | Leu | Pro | Phe | His | Glu | Ile | Ile | Gly | Lys |      |
| 329 |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |     |      |
| 332 | ata | ttg | aat | tac | cgg | cag | ctt | atg | aag | tta | aaa | tcc | act | tat | act | gac | 960  |
| 333 | Ile | Leu | Asn | Tyr | Arg | Gln | Leu | Met | Lys | Leu | Lys | Ser | Thr | Tyr | Thr | Asp |      |
| 334 | 305 |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |     |      |
| 336 | ggc | tta | atg | cct | tta | ata | aat | gag | cgt | acc | ggt | aaa | ctt | cac | act | act | 1008 |
| 337 | Gly | Leu | Met | Pro | Leu | Ile | Asn | Glu | Arg | Thr | Gly | Lys | Leu | His | Thr | Thr |      |
| 338 |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |     |      |
| 340 | ttt | aac | cag | acc | ggt | act | tta | acc | gga | cgc | ctg | gcg | tct | tcg | gag | ccc | 1056 |
| 341 | Phe | Asn | Gln | Thr | Gly | Thr | Leu | Thr | Gly | Arg | Leu | Ala | Ser | Ser | Glu | Pro |      |
| 342 |     |     | 340 |     |     |     |     |     | 345 |     |     |     | 350 |     |     |     |      |
| 344 | aat | ctc | caa | aat | att | ccc | atc | cgg | ttg | gaa | ctc | ggt | cgg | aaa | tta | cgc | 1104 |
| 345 | Asn | Leu | Gln | Asn | Ile | Pro | Ile | Arg | Leu | Glu | Leu | Gly | Arg | Lys | Leu | Arg |      |
| 346 |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |     |      |
| 348 | aag | atg | ttt | ata | cct | tca | ccg | ggg | tat | gat | tat | att | gtt | tcg | gcg | gat | 1152 |
| 349 | Lys | Met | Phe | Ile | Pro | Ser | Pro | Gly | Tyr | Asp | Tyr | Ile | Val | Ser | Ala | Asp |      |
| 350 |     | 370 |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |     |      |
| 352 | tat | tcc | cag | att | gaa | tta | agg | ctt | ctt | gcc | cat | ttt | tcc | gaa | gag | ccc | 1200 |
| 353 | Tyr | Ser | Gln | Ile | Glu | Leu | Arg | Leu | Leu | Ala | His | Phe | Ser | Glu | Glu | Pro |      |
| 354 | 385 |     |     |     | 390 |     |     |     |     | 395 |     |     |     | 400 |     |     |      |
| 356 | aag | ctt | att | gaa | gct | tac | caa | aaa | ggg | gag | gat | att | cac | cgg | aaa | acg | 1248 |
| 357 | Lys | Leu | Ile | Glu | Ala | Tyr | Gln | Lys | Gly | Glu | Asp | Ile | His | Arg | Lys | Thr |      |
| 358 |     |     | 405 |     |     |     |     |     | 410 |     |     |     | 415 |     |     |     |      |
| 360 | gcc | tcc | gag | gtg | ttc | ggt | gta | tct | ttg | gaa | gaa | gtt | act | ccc | gag | atg | 1296 |
| 361 | Ala | Ser | Glu | Val | Phe | Gly | Val | Ser | Leu | Glu | Glu | Val | Thr | Pro | Glu | Met |      |
| 362 |     |     | 420 |     |     |     |     |     | 425 |     |     |     | 430 |     |     |     |      |
| 364 | cgc | gct | cat | gcc | aag | tcg | gtg | aac | ttc | ggc | att | gtt | tat | ggc | att | agt | 1344 |
| 365 | Arg | Ala | His | Ala | Lys | Ser | Val | Asn | Phe | Gly | Ile | Val | Tyr | Gly | Ile | Ser |      |

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366          435          440          445
368 gat ttt ggt tta ggc aga gac tta aag att ccc cgg gag gtt gcc ggt      1392
369 Asp Phe Gly Leu Gly Arg Asp Leu Lys Ile Pro Arg Glu Val Ala Gly
370          450          455          460
372 aag tac att aaa aat tat ttt gcc aac tat ccc aaa gtg cgg gag tat      1440
373 Lys Tyr Ile Lys Asn Tyr Phe Ala Asn Tyr Pro Lys Val Arg Glu Tyr
374 465          470          475          480
376 ctc gat gaa ctt gtc cgt acg gca aga gaa aag gga tat gtg acc act      1488
377 Leu Asp Glu Leu Val Arg Thr Ala Arg Glu Lys Gly Tyr Val Thr Thr
378          485          490          495
380 tta ttt ggg cga aga cgc tat att cct gag cta tct tca aaa aac cgc      1536
381 Leu Phe Gly Arg Arg Arg Tyr Ile Pro Glu Leu Ser Ser Lys Asn Arg
382          500          505          510
384 acg gtt cag ggt ttt ggc gaa agg acg gcc atg aat act ccc ctt cag      1584
385 Thr Val Gln Gly Phe Gly Glu Arg Thr Ala Met Asn Thr Pro Leu Gln
386          515          520          525
388 ggc tcg gct gcc gat att att aag ctt gca atg att aat gta gaa aaa      1632
389 Gly Ser Ala Ala Asp Ile Ile Lys Leu Ala Met Ile Asn Val Glu Lys
390          530          535          540
392 gaa ctt aaa gcc cgt aag ctt aag tcc cgg ctc ctt ctt tcg gtg cac      1680
393 Glu Leu Lys Ala Arg Lys Leu Lys Ser Arg Leu Leu Leu Ser Val His
394 545          550          555          560
397 gat gag tta gtt tta gaa gtg ccg gcg gaa gag ctg gaa gag gta aaa      1728
398 Asp Glu Leu Val Leu Glu Val Pro Ala Glu Glu Leu Glu Glu Val Lys
399          565          570          575
401 gcg ctg gta aaa ggg gtt atg gag tcg gtg gtt gaa ctg aaa gtg cct      1776
402 Ala Leu Val Lys Gly Val Met Glu Ser Val Val Glu Leu Lys Val Pro
403          580          585          590
405 tta atc gct gaa gtt ggt gca ggc aaa aac tgg tat gaa gcg aag taa      1824
406 Leu Ile Ala Glu Val Gly Ala Gly Lys Asn Trp Tyr Glu Ala Lys
407          595          600          605
410 <210> SEQ ID NO: 11
412 <211> LENGTH: 607
414 <212> TYPE: PRT
416 <213> ORGANISM: Carboxydothermus hydrogenoformans
420 <400> SEQUENCE: 11
422 Met Glu Lys Leu Ala Glu His Glu Asn Leu Ala Lys Ile Ser Lys Gln
423 1          5          10          15
426 Leu Ala Thr Ile Leu Arg Glu Ile Pro Leu Glu Ile Ser Leu Glu Asp
427          20          25          30
430 Leu Lys Val Lys Glu Pro Asn Tyr Glu Glu Val Ala Lys Leu Phe Leu
431          35          40          45
434 His Leu Glu Phe Lys Ser Phe Leu Lys Glu Ile Glu Pro Lys Ile Lys
435          50          55          60
438 Lys Glu Tyr Gln Glu Gly Lys Asp Leu Val Gln Val Glu Thr Val Glu
439 65          70          75          80
442 Thr Glu Gly Gln Ile Ala Val Val Phe Ser Asp Gly Phe Tyr Val Asp
443          85          90          95
446 Asp Gly Glu Lys Thr Lys Phe Tyr Ser Leu Asp Arg Leu Asn Glu Ile

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## VERIFICATION SUMMARY

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Input Set : A:\1803.txt

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L:23 M:270 C: Current Application Number differs, Replaced Current Application No  
L:23 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:49 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1  
L:78 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:87 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2  
L:106 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:115 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3  
L:133 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4  
L:151 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5  
L:169 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6  
L:187 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7  
L:205 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8  
L:223 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9  
L:583 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12